

FIGURE 1

```

1  AGCTCCAGCCTAGGCGTTCTACCTGGAAGAAATGCAGGGGCCAGTACCTAGGACTGAGGA      60
61  AGATGGCTGACATCCAGAAACAATTTCGCTGGACAGCCAGGAGCGTAGGGCTGTGGCAG      120
180  TGCCTGTGATCTTTGCCCTCAATCTCCCTGTTGGGCAATGGTGGCAATGGGCTGGTGTGG      180
240  CTGTGCTACTGCAGCCTGGCCCAAGTGCCCTGGCAGAGCCAAAGCAGTACCACAGATCTCT      240
300  TCATCCTCAACTTGGCCGTGGCCGACCTTTGCTTCAATCCTGTGCTGCGTGCCCTTCCAGG      300
360  CAGCCATCTACACACTGGATGCCCTGGCTCTTTGGGCTTTCTGTGTGCAAGACGGTACATC      360
420  TGCTCATCTACCTACCATGTATGCCAGCAGCTTACCCCTGGCGGCGTCTCCCTGGACA      420
480  GTACCTGGCTGTGGCGCACCCACTGGGCTCCAGAGCCCTGCGCACCCCGGCAACGCGC      480
540  GCGCGCCGTGGGCTCGTGTGGCTGCTGGCGGCTCTCTTTCCGCGCCCTACCTAAGCT      540
600  ATTACGGCACGGTGCGCTACGGCGGCTCGAGCTCTGCGTGCCCGCTTGGGAGGACGCGC      600
660  GGCGCGCGCGCTGGACGTGGCCACCTTCGCCCGGGCTACCTGCTGCCGTGCCGTGGCGG      660
720  TGAGCCTGGCTACGGACGACGCTATGTTTCTATGGCGCGCGTGGGTCCCGCGGCGG      720
780  CGCGGCGCAGAGCGCGCAGACGGCGACCGCGCGGGGACGCGCCATGCTGGCAG      780
840  TGGCCGCGCTTACGCGCTTGTGCGGCGCCGACACGCGCTCATCTCTGCTTCTGGT      840
900  ACGCGCGCTTCGCGCTTACGCGCGCCACCTACGCTGTGCGCTTGGCCTCGCACCTGCC      900
960  CCTACGCCAACTCCTGCCCTTAACCCGCTCGGCTTACTCGCTCGCTCGCGCCACTTCCG      960
1020  CGCGCTTCCGCGCGCTGTGGCCCTTCGCGCGCTCGCGCCACCGCCACACCGCGCTC      1020
1080  ATCGAGCCCTCCGTCGTGTCCAGCCGGCGTCTTCGGGCCCCCGCGGTATATCCCGCG      1080
1140  CCAGGCTTCCGTCGTGTGGAGTATGGAGCCAGAGGGATGCTCTGCGTGGTGGAGAGA      1140
1200  CTAGACTAACCTGTCCCCCAGGGACCTCAATAACCCCTGCCCGCTTGGACTCTGACGTC      1200
1260  TGTCAGAATGCCACCAAGGAACAATAGGGAACGGCAGTCTCGCCAGGCTCCACCAAAA      1260
1280  GCAGAAGCAAAAGTTGCAGGG

```

FIGURE 2

20	V	A	F	A	L	R	R	Y	R	V	A	V	Y	A	A	H	A	T
40	A	L	L	Q	H	D	A	S	A	V	G	A	W	L	R	A	D	E
60	V	V	D	F	V	L	N	L	D	A	A	L	F	C	F	R	G	G
80	A	L	T	P	T	S	R	Y	E	V	P	M	C	H	H	H	P	G
100	G	G	T	V	K	V	P	P	W	P	G	A	L	S	R	H	Y	G
120	V	N	S	C	C	A	T	A	A	L	V	R	I	A	S	H	G	R
140	S	G	S	C	V	A	R	S	P	L	A	G	L	L	A	R	A	L
160	G	V	P	L	F	L	L	F	V	Y	A	A	A	R	L	H	P	A
180	P	M	E	I	A	T	A	L	C	G	W	R	H	C	S	R	G	D
200	S	G	Q	F	G	F	R	A	L	A	L	G	H	A	Y	R	S	G
220	D	L	W	C	F	S	S	A	E	A	F	T	P	Y	V	R	S	R
240	L	L	A	L	L	S	R	L	L	F	C	A	G	T	L	G	A	P
260	S	F	S	D	W	A	L	L	A	T	L	R	W	A	P	C	P	E
280	I	I	P	A	A	Y	P	W	G	A	T	R	C	P	N	P	Q	M
300	N	L	G	V	D	M	H	V	Y	V	R	R	L	S	L	W	V	S
320	Q	A	P	A	L	T	R	L	R	D	G	A	A	F	C	L	R	W
340	I	F	Q	L	T	L	V	G	V	L	Y	E	Y	A	S	R	R	G
360	D	I	L	N	Y	Y	A	V	T	A	A	A	L	F	N	R	L	R
370	A	V	L	L	I	I	L	A	G	R	L	A	A	R	A	F	A	P
	M	P	V	I	A	L	Y	A	Y	R	S	A	A	G	Y	R	R	R

FIGURE 3

1	CAC	60
61	AGAA	120
21	GGGG	180
81	GCTGA	240
141	GTGGT	300
201	CTCCT	360
261	CTCA	420
321	ATCTA	480
381	ATCTA	540
	CTGG	600
	GCAG	660
	GGCA	720
	GGCA	780
	CGGC	840
	CTGG	900
	GCGC	960
	GCGC	1020
	CGCT	1080
	GCCA	1140
	TTCG	1200
	CGCG	1260
	AGGC	1320
	GAGG	1380
	TCAC	1417
	TCTC	

FIGURE 4

1	P	20
21	T	40
41	M	60
61	P	80
81	V	100
01	I	120
21	T	140
41	L	160
61	Y	180
81	A	200
01	Y	220
21	R	240
41	S	260
61	A	280
81	A	300
01	G	320
21	Y	340
41	R	360
61	R	380
81	G	400
01	G	420
21		440

Q R E V A F A L R R Y R V A V Y A A L S G
 F T G A L L Q H D A S A V G A W L R A P H
 S A D V V D F V V N L D A A L F C F R R V
 T Q S A L T P A S R Y E V P M C H H R A P
 P G P G G T V K V P P W P G A L S R A D G
 S R C V N S C C A T A A L V R I A S R G E
 P S R S G G C V A R S P L A G L L A H P R
 P R P G V P L L L L F V Y A A A R L R C P
 P V L P T E I A T A L C G W R H C A R G E
 S G S S G Q F G F R A L A L G H A Y R P P
 L G A D L W C F S S A E A F T P Y V R P G
 L V P L L A L L S R L L F R A G T L G G Q
 A Q I S F S D W A L L A T L R W A P C S G E
 L T R I I P A A Y P W G A T R C P N P S G P
 T Q L N L G V D M H V Y V R R L S L W A G G
 M G C Q A P A L T R L R D G A A F C L P A R
 A P S A F Q L T L V G V L Y E Y A S R R R L A
 S T G D V L N Y Y A V T A A A L F N R V L A
 H R G A V L L I I L A G R L A A R A F R R E

FIGURE 5A

hGALR3	M A D A Q N I S L D S P G	13
rGALR3	M A D I Q N I S L D S P G	13
rGALR1	M E L A P V N L S E G N G S D P E P P A E P R P L		25
I			
hGALR3	. . . S V G A V A V P V V F A L I F L L G T V G N		35
rGALR3	. . . S V G A V A V P V I F A L I F L L G M V G N		35
rGALR1	F G I G V E N F I T L V V F F G L I F A M G V L G N		50
II			
hGALR3	G L V L A V L L Q P G P S A W Q E P G S T T D L F		60
rGALR3	G L V L A V L L Q P G P S A W Q E P S S T T D L F		60
rGALR1	S L V I T V L A R S K P G . . . K P R S T T N L F		72
II			
hGALR3	I L N L A V A D L C F I L C C V P F Q A T I Y T L		85
rGALR3	I L N L A V A D L C F I L C C V P F Q A A I Y T L		85
rGALR1	I L N L S I A D L A Y L L F C I P F Q A T V Y A L		97

	III																									
hGALR3	D	A	W	L	F	G	A	L	V	C	K	A	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR3	D	A	W	L	F	G	A	F	V	C	K	T	V	H	L	L	I	Y	L	T	M	Y	A	S	S	110
rGALR1	P	T	W	V	L	G	A	F	I	C	K	F	I	H	Y	F	F	T	V	S	M	L	V	S	I	122
hGALR3	F	T	L	A	A	V	S	V	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR3	F	T	L	A	A	V	S	L	D	R	Y	L	A	V	R	H	P	L	R	S	R	A	L	R	T	135
rGALR1	F	T	L	A	A	M	S	V	D	R	Y	V	A	I	V	H	S	R	R	S	S	L	R	V	147	
hGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR3	P	R	N	A	R	A	A	V	G	L	V	W	L	L	A	A	L	F	S	A	P	Y	L	S	Y	160
rGALR1	S	R	N	A	L	L	G	V	G	F	I	W	A	L	S	I	A	M	A	S	P	.	V	A	Y	171
hGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR3	Y	G	T	V	.	.	R	Y	G	A	L	E	L	C	V	P	A	W	.	E	D	A	R	R	R	182
rGALR1	Y	Q	R	L	F	H	R	D	S	N	Q	T	F	C	W	E	H	W	P	N	Q	L	H	K	K	196

FIGURE 5C

hGALR3 rGALR3 rGALR1	V															207 207 221									
	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	S	L	A	Y	G	R	T	
	A	L	D	V	A	T	F	A	A	G	Y	L	L	P	V	A	V	S	L	A	Y	G	R	T	
	A	Y	V	V	C	T	F	V	F	G	Y	L	L	P	L	L	I	C	F	C	Y	A	K	V	
hGALR3 rGALR3 rGALR1	VI															232 232 242									
	L	R	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	A	T	G	R		
	L	C	F	L	W	A	A	V	G	P	A	G	A	A	A	E	A	R	R	A	T	G	R		
	L	N	H	L	H	K	K	L	K	N	M	S	K	K	S	E	A	S	K	.	.	.	K		
hGALR3 rGALR3 rGALR1	VII															257 257 267									
	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C
	A	G	R	A	M	L	A	V	A	A	L	Y	A	L	C	W	G	P	H	H	A	L	I	L	C
	T	A	Q	T	V	L	V	V	V	V	V	F	G	I	S	W	L	P	H	H	V	I	H	L	W
hGALR3 rGALR3 rGALR1	VIII															282 282 292									
	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A
	F	W	Y	G	R	F	A	F	S	P	A	T	Y	A	C	R	L	A	S	H	C	L	A	Y	A
	A	E	F	G	A	F	P	L	T	P	A	S	F	F	F	R	I	T	A	H	C	L	A	Y	S

FIGURE 5D

hGALR3	N	S	C	L	N	P	L	V	Y	A	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR3	N	S	C	L	N	P	L	V	Y	S	L	A	S	R	H	F	R	A	R	F	R	R	L	W	P	307
rGALR1	N	S	S	V	N	P	I	I	Y	A	F	L	S	E	N	F	R	K	A	Y	K	Q	V	F	K	317
hGALR3	C	G	R	R	R	.	.	.	R	H	R	A	R	R	A	L	R	R	V	R	P	A	S	S	G	329
rGALR3	C	G	R	R	R	H	R	H	H	R	A	H	R	A	L	R	R	V	Q	P	A	S	S	G	332	
rGALR1	C	R	V	C	N	E	S	P	H	G	D	A	K	E	K	N	R	I	D	T	P	P	S	T	N	342
hGALR3	P	P	G	C	P	G	D	A	R	P	S	G	R	L	L	A	G	G	Q	G	P	E	P	R	354	
rGALR3	P	A	G	Y	P	G	D	A	R	P	R	G	W	S	M	E	P	R	350		
rGALR1	C	T	H	V	346	
hGALR3	E	G	P	V	H	G	G	E	A	A	R	G	P	E	.	.	.	368		
rGALR3	G	D	A	L	R	G	G	E	T	R	L	T	L	S	P	R	G	P	Q	370		

FIG. 6A

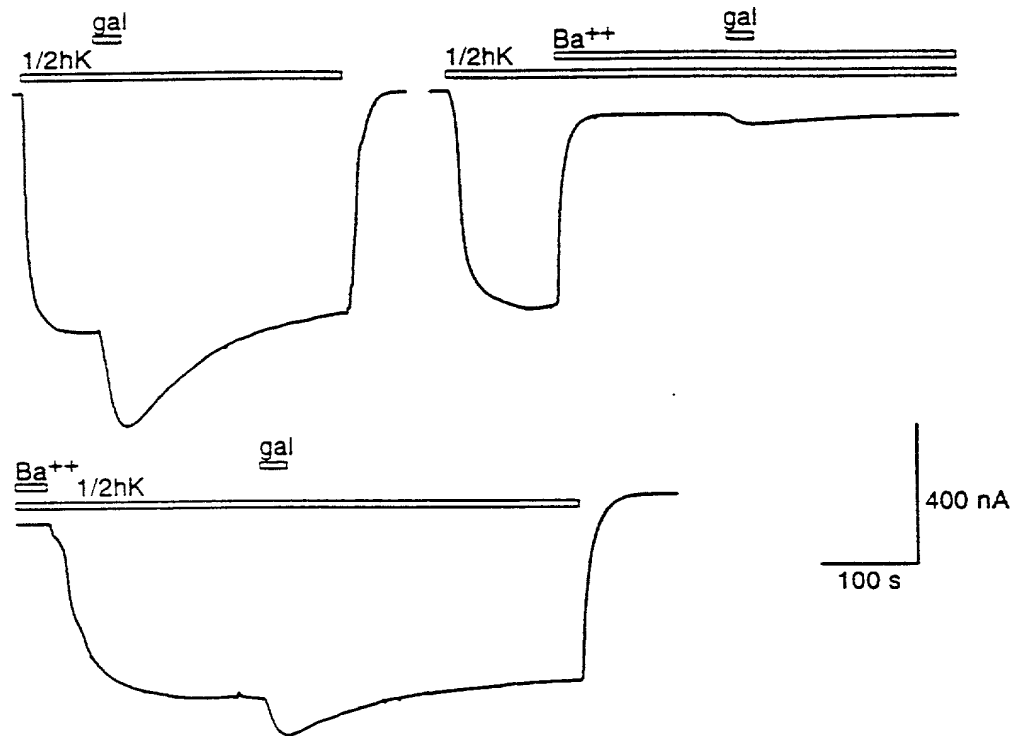


FIG. 6B

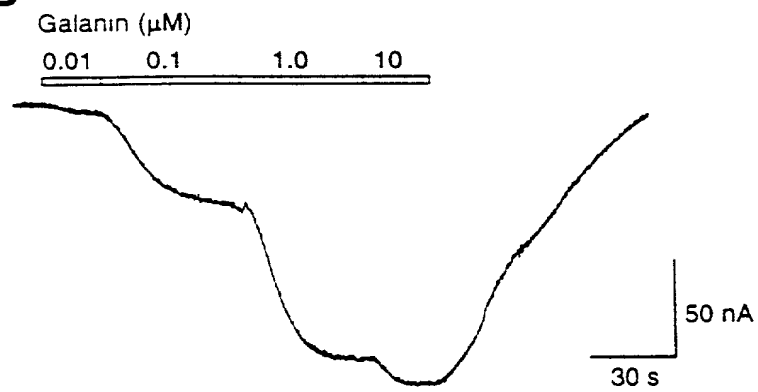
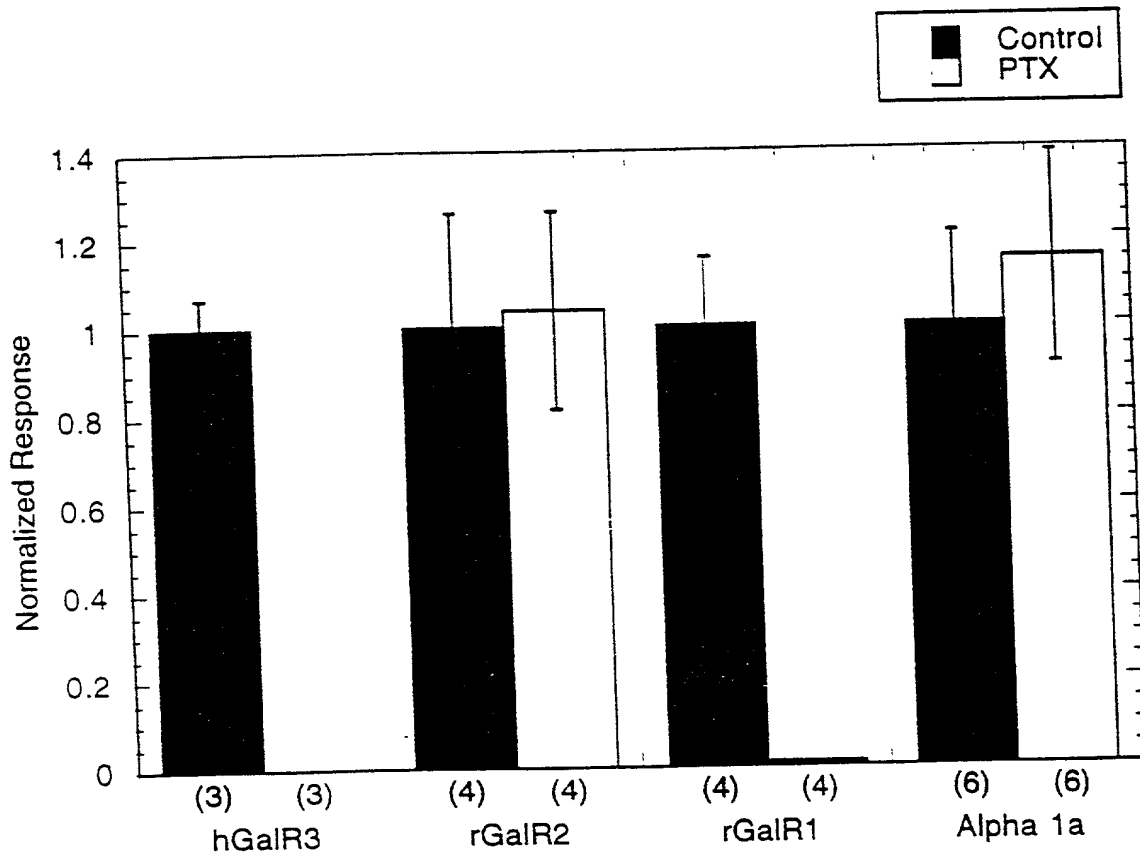


FIG. 7



11/19

FIG. 8A

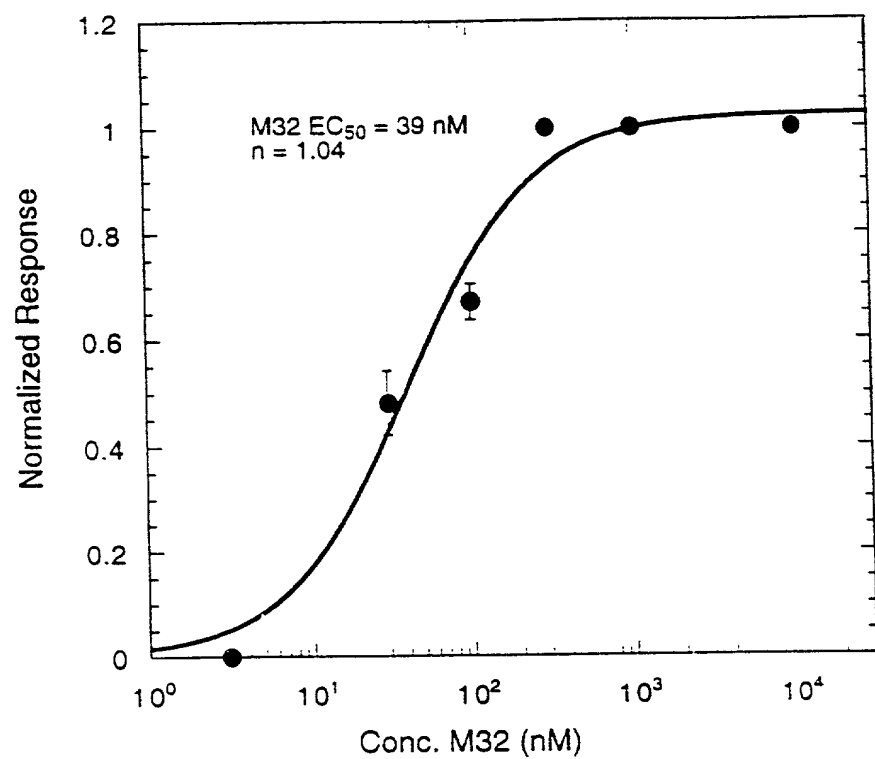


FIG. 8B

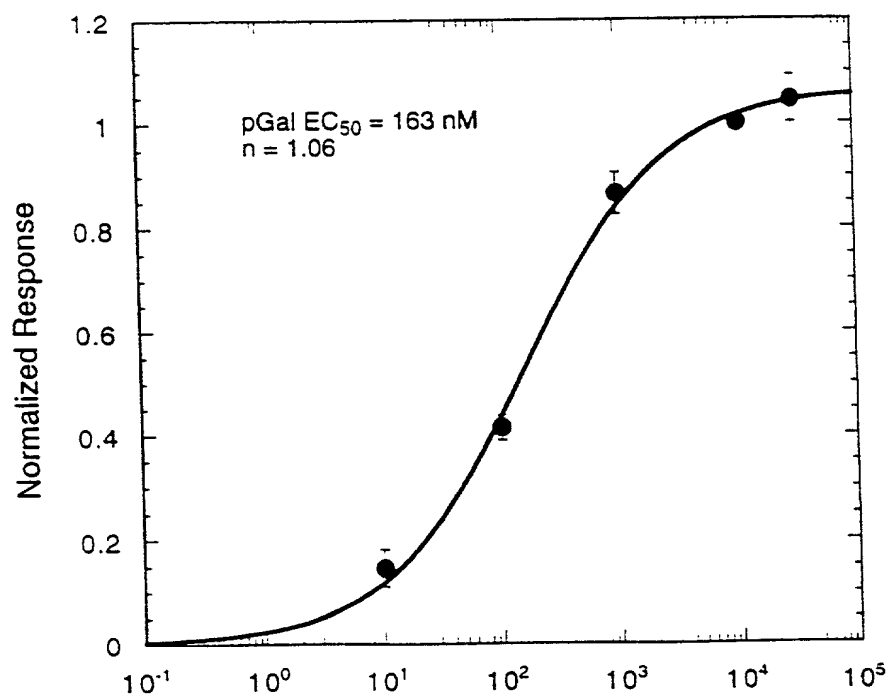


FIG. 8C

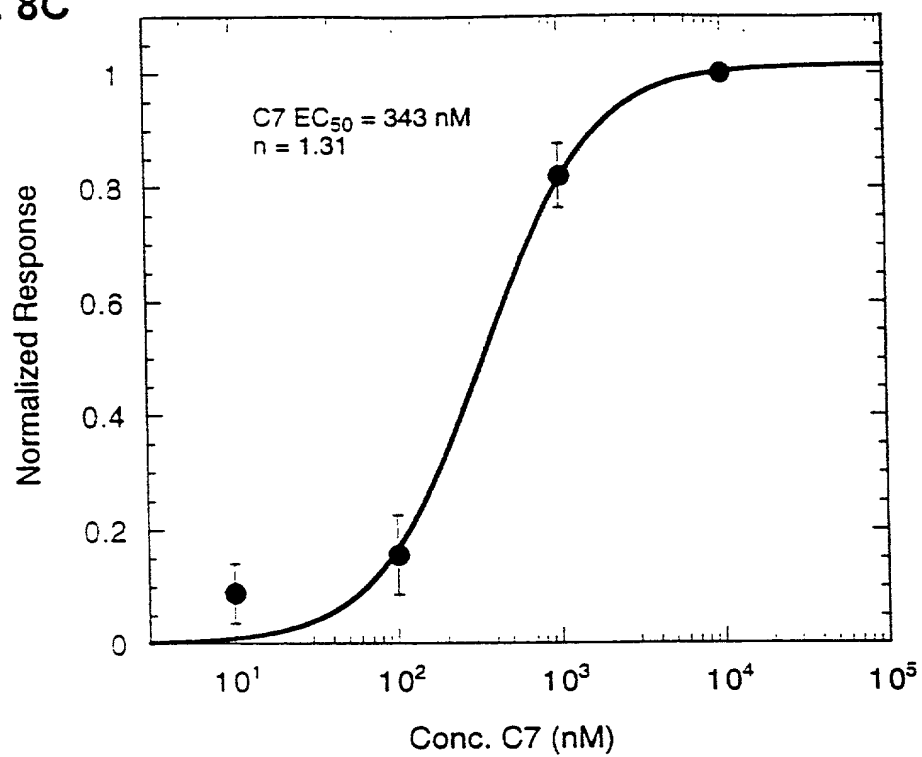


FIG. 8D

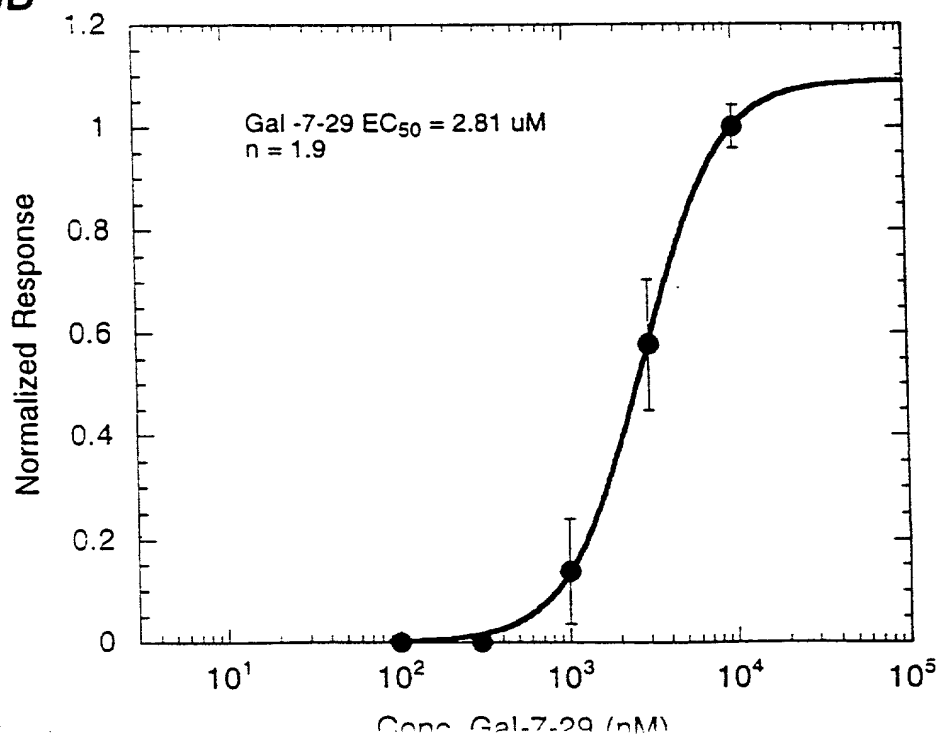


FIG. 8E

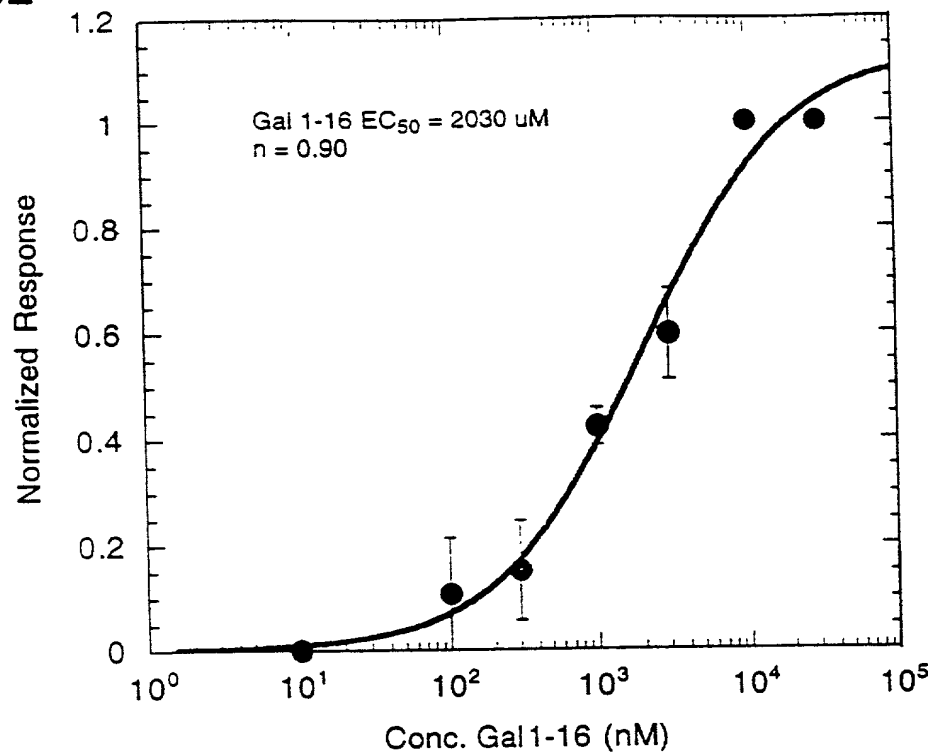


FIG. 8F

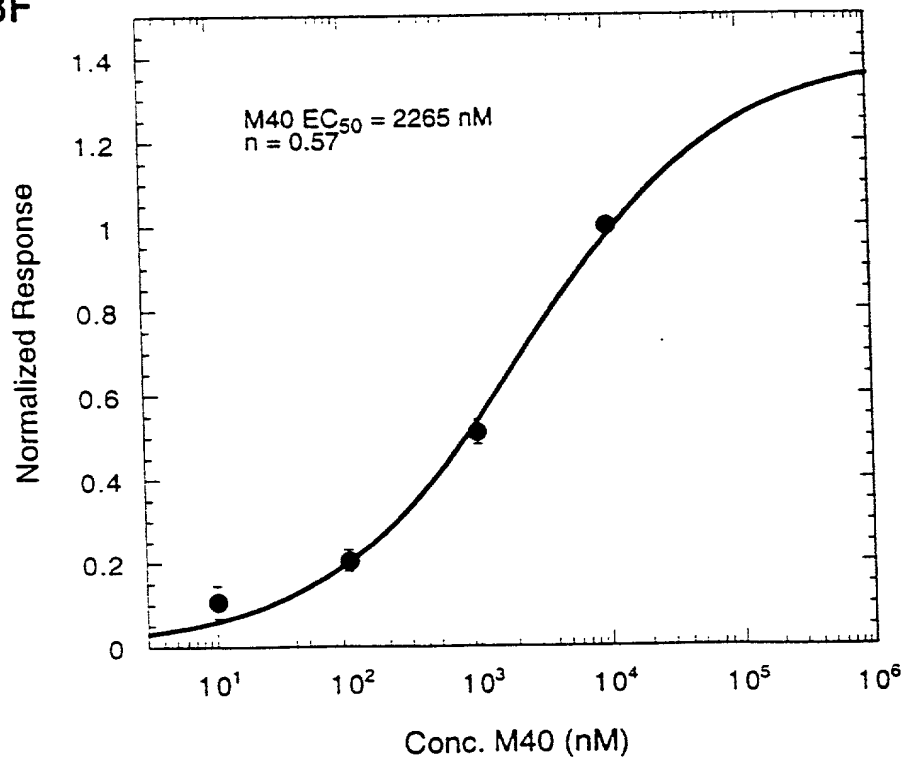


FIG. 9A

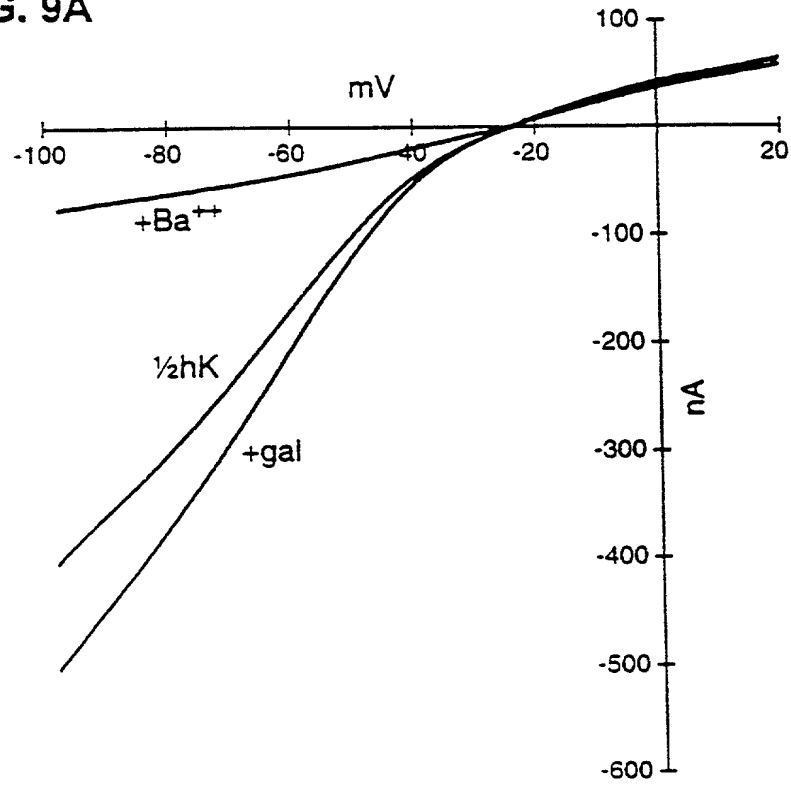


FIG. 9B

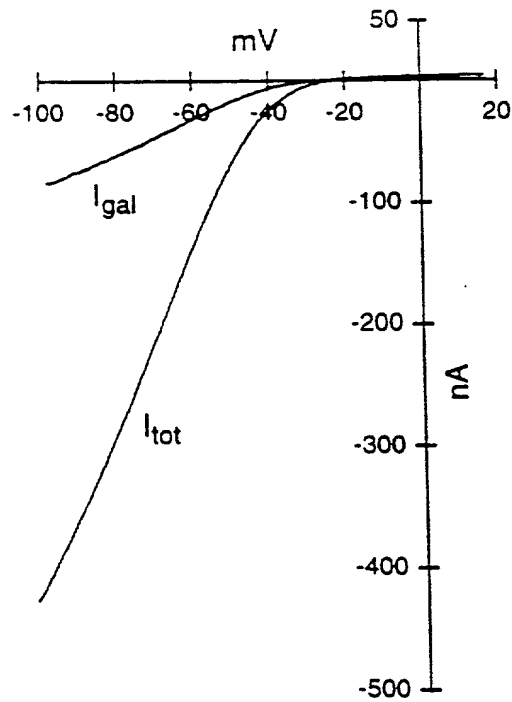


FIG. 10

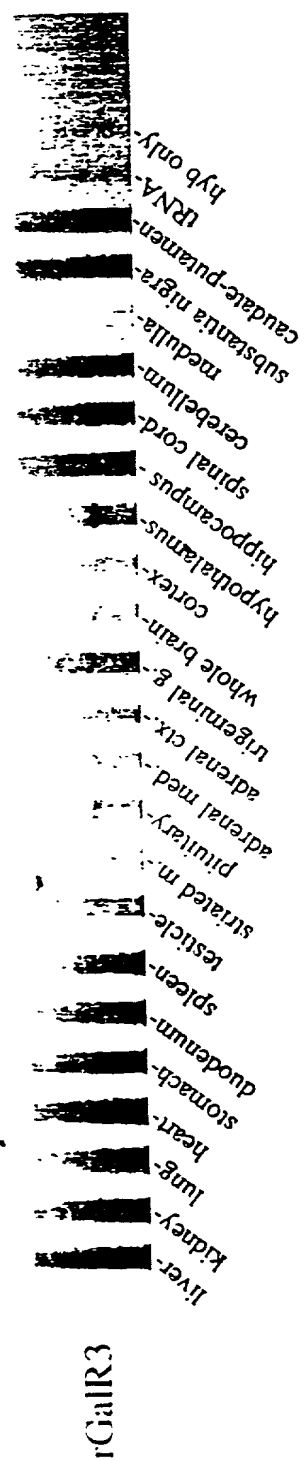


FIG. 11

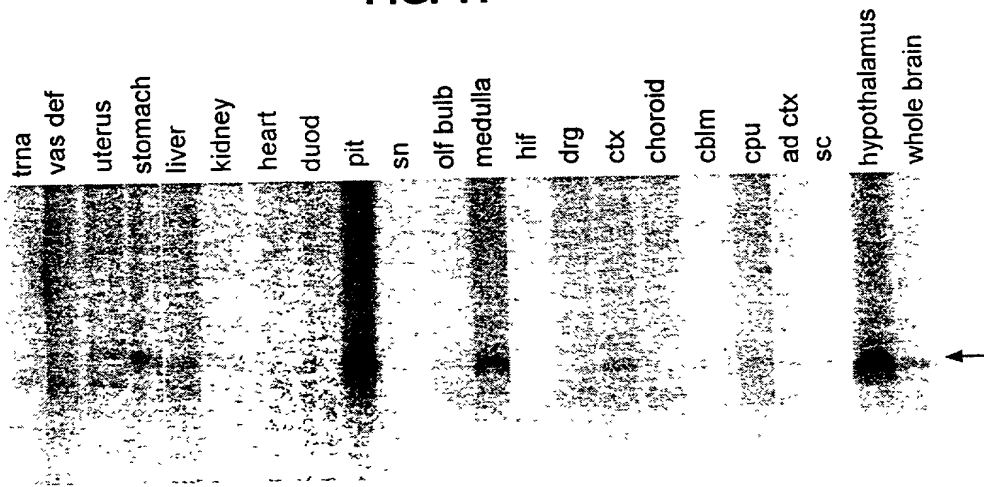


FIG. 12

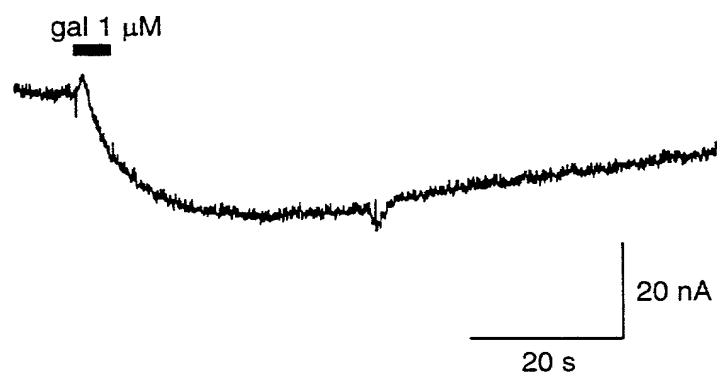


FIG. 13A

hGALR3-LM #228 **+/- Pertussis Toxin**

Guanine nucleotide effects

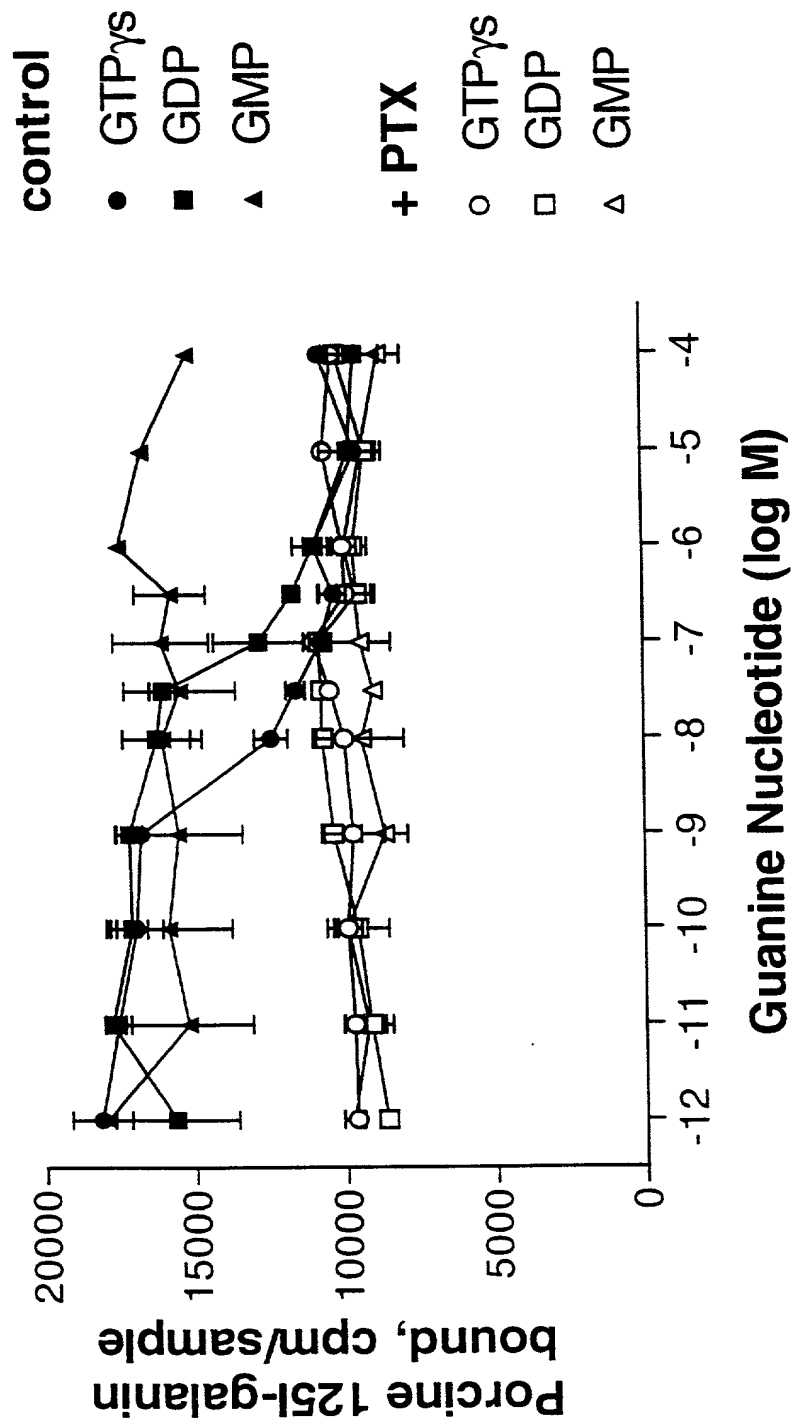


FIG. 13B

Nonspecific Binding
with 1 μ M p galanin

